WHAT IS CLAIMED:

1. In a computer system, a method of sequencing a nucleic acid sequence, the method comprising the steps of:

inputting hybridization intensities into a computer for a plurality of nucleic acid probes, the nucleic acid probes hybridizing with the nucleic acid sequence under conditions that do not allow identification of all nucleic acid probes that are perfectly complementary to part of the nucleic acid sequence; and

sequencing the nucleic acid sequence according to selected nucleic acid probes.

2. The method of claim 1, further comprising the step of selecting nucleic acid probes utilizing mismatch information among the nucleic acid probes.

3. The method of claim 1, further comprising the step of selecting nucleic acid probes with the highest numbers of single base mismatch neighbors among the probes, a single base mismatch neighbor being another probe that has the same sequence except for a single base that is different.

4. The method of claim 1, further comprising the step of selecting nucleic acid probes that have fewer than a predetermined number of base mismatches with another probe.

5. The method of claim 1, further comprising the step of selecting nucleic acid probes with highest hybridization intensities.

6. The method of claim 5, wherein the nucleic acid probes with the highest hybridization intensities are above an intensity threshold.

7. The method of claim 1, wherein the sequencing step includes the steps of:

aligning the selected nucleic acid probes so that bases that are common overlap; and

sequencing the nucleic acid sequence according to bases that occur most often at each position in the aligned nucleic acid probes.

8. The method of claim 7, wherein the nucleic acid sequence is sequenced as complementary to the bases that occur most often.

9. A computer program product that sequences a nucleic acid sequence, comprising:

computer readable code that receives as input hybridization intensities for a plurality of nucleic acid probes, the nucleic acid probes hybridizing with the nucleic acid sequence under conditions that do not allow identification of all nucleic acid probes that are perfectly complementary to part of the nucleic acid sequence; and

computer readable code that sequences the nucleic acid sequence according to selected nucleic acid probes;

wherein the computer readable code are stored on a tangible medium.